

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:59:39 ; Search time 11 Seconds  
(without alignments)  
56.559 Million cell updates/sec

Title: US-09-300-612-1

Perfect score: 84

Sequence: 1 LKAMDPTPLWKTE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	291	DM43_DIDMR	P29577 didelphis m
2	47	56.0	351	Y4VJ_RHISN	Q53218 rhizobium s
3	46	54.8	1213	T2D2_DROME	Q24325 drosophila
4	44	52.4	777	YASB_SCHPO	Q10146 schizosacch
5	44	52.4	1305	RRPL_AHSV9	Q70695 african hor
6	43	51.2	341	NAGZ_SALTY	Q82716 salmonella
7	43	51.2	341	NAGZ_SALTY	Q82716 salmonella
8	43	51.2	932	RMDH_STRPU	P63393 strongyloce
9	42	50.0	398	Y306_CHLMO	Q91022 chlamydia m
10	42	50.0	453	AAT5_ARATH	P46248 arabidopsis
11	42	50.0	564	NCAP_MACHU	P26578 machupo vir
12	42	50.0	662	FASL_SCHAM	P10675 schistocerc
13	41	48.8	151	RS13_MAIZE	Q05761 zea mays (m
14	40	47.6	151	RS13_AGABI	P78571 agarcus bi
15	40	47.6	209	Y5CK_YEREN	Q01252 versinia en
16	40	47.6	209	Y5CK_YERPE	Q00927 versinia en
17	40	47.6	225	CSSR_BACSU	Q32192 bacillus su
18	40	47.6	231	YRKP_BACSU	P54443 bacillus su
19	40	47.6	344	DCUP_RHOCA	P42503 rhodobacter
20	40	47.6	1184	ALAC_ARATH	P57792 arabidopsis
21	39.5	47.0	615	CNK_RAT	Q39011 rattus norv
22	39.5	47.0	631	CNK_MOUSE	Q60806 mus musculu
23	39.5	47.0	646	CNK_HUMAN	Q944b4 homo sapien
24	39	46.4	256	US02_PRVN3	P24382 pseudorabie
25	39	46.4	268	VG65_BPML5	Q05279 mycobacteri
26	39	46.4	412	BHB2_HUMAN	Q14503 homo sapien
27	39	46.4	700	PHLN_BURPS	Q7988 burkholderi
28	39	46.4	936	YNG2_CAEEL	Q21653 caenorhabdi
29	38.5	45.8	401	RENS_MOUSE	P00796 mus musculu
30	38.5	45.8	402	RENI_MOUSE	P06281 mus musculu
31	38.5	45.8	450	TLLD_DROVI	Q16845 drosophila
32	38.5	45.8	452	TLLD_DROME	P18102 drosophila
33	38	45.2	192	Y4PG_RHISN	P55616 rhizobium s

34	38	45.2	387	1	MANA_RHIME	P29954 rhizobium m
35	38	45.2	453	1	MTE1_MOUSE	Q93979 mus musculu
36	38	45.2	542	1	YQ16_CAEEL	Q09279 caenorhabdi
37	38	45.2	867	1	YK2A_CAEEL	P34447 caenorhabdi
38	38	45.2	1202	1	ALAA_ARATH	Q91183 arabidopsis
39	38	45.2	1325	1	YAE6_SCHPO	Q09847 schizosacch
40	38	45.2	1443	1	E75C_DROME	P13055 drosophila
41	38	45.2	1815	1	SHK3_RAT	Q911u4 rattus norv
42	37.5	44.6	362	1	KLF1_HUMAN	P13351 homo sapien
43	37.5	44.6	825	1	ICP0_HSV2H	P28284 herpes simp
44	37	44.0	102	1	YC4_TYLCA	P36283 tomato yell
45	37	44.0	142	1	MNTR_LISIN	Q92ad1 listeria in

#### ALIGNMENTS

##### RESULT 1

ID	DM43_DIDMR	STANDARD;	PRT;	291 AA.
AC	P82957;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Venom metalloproteinase inhibitor DM43.			
OS	Didelphis marsupialis (Southern opossum).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.			
OX	NCBI_TaxID=9268;			
RN	(1)			
RP	SEQUENCE, AND MASS SPECTROMETRY.			
RC	TISSUE=Serum;			
RX	MEDLINE=21935368; PubMed=11815628;			
RA	Neves-Ferreira A.G.C.; Perales J.; Fox J.W.; Shannon J.D.;			
RA	Makino D.I.; Garratt R.C.; Domont G.B.;			
RT	"Structural and functional analyses of DM43, a snake venom			
RT	metalloproteinase inhibitor from Didelphis marsupialis serum.";			
RL	J. Biol. Chem. 277:13129-13137(2002).			
CC	- FUNCTION: Metalloproteinase inhibitor.			
CC	- SUBUNIT: Homodimer.			
CC	- TISSUE SPECIFICITY: Blood and milk.			
CC	- PTM: N-Glycosylated.			
CC	- MASS SPECTROMETRY: MW=42691; METHOD=MALDI.			
CC	- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.			
CC	- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.			
DR	InterPro: IPR003599; Ig.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003600; Ig_like.			
DR	SMART: SM00409; Ig; 2.			
DR	SMART: SM00410; Ig like; 1.			
KW	Metalloprotease inhibitor; Venom; Glycoprotein; Repeat;			
KW	Immunoglobulin domain.			
FT	DOMAIN 22 79			
FT	DOMAIN 114 171			
FT	DOMAIN 206 272			
FT	DISULFID 28 74			
FT	DISULFID 121 163			
FT	DISULFID 213 265			
FT	CARBOHYD 23 23			
FT	CARBOHYD 156 156			
FT	CARBOHYD 160 160			
FT	CARBOHYD 175 175			
FT	SEQUENCE 291 AA; 32390 MW; 17A496227E69A65B CRC64;			

Query Match 100.0%; Score 84; DB 1; Length 291;

Best Local Similarity 100.0%; Pred. No. 3.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWKTE 15

Db 1 LKAMDPTPLWKTE 15

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RESULT 2
Y4VJ_RHISN
ID Y4VJ_RHISN STANDARD; PRT; 351 AA.
AC Q53218;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 39.2 kDa protein Y4VJ.
GN Y4VJ.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freilberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RT Perret X.;
RL "Molecular basis of symbiosis between Rhizobium and legumes.";
RN [2]
RP SEQUENCE OF 1-279 FROM N.A.
RX MEDLINE=96389014; PubMed=8796346;
RA Freilberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT NGR234 using dye terminators and a thermostable 'sequenase': a
RT beginning.";
RL Genome Res. 6:590-600(1996).
CC -1- SIMILARITY: TO ALKANAL MONOOXYGENASE ALPHA AND BETA CHAINS (EC
CC 1.14.14.3) (BACTERIAL LUCIFERASE). BUT DISTANTLY RELATED.
CC -1- SIMILARITY: TO Y4WF.
CC
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CC
DR EMBL: Z68203; CAA92425.1;
DR EMBL: AE000101; BAB1898.1;
DR InterPro: IPR002103; Bac_Luciferase.
DR Pfam: PF00296; bac_Luciferase; 1.
KW Hypothetical protein; Oxidoreductase; Monooxygenase; Plasmid.
SQ SEQUENCE 351 AA; 39158 MW; 866BDE3B8A40C88D CRC64;

Query Match 56.0%; Score 47; DB 1; Length 351;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FTPLPWIKT 14
DB 167 FTPLPWIKT 175

RESULT 3
T2D2_DROME
ID T2D2_DROME STANDARD; PRT; 1213 AA.
AC Q24325;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Transcription initiation factor TFIID 150 kDa subunit (TAFII-150)
DE (TAFII150).
GN TAF150
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

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RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=94233377; PubMed=8178153;
RA Verrijzer C.P., Yokomori K., Chen J.-L., Tjian R.;
RT "Drosophila TAFII150: similarity to yeast gene TSM-1 and specific
RT binding to core promoter DNA.";
RL Science 264:933-941(1994).
CC -1- FUNCTION: TAFs ARE COMPONENTS OF THE TRANSCRIPTION FACTOR IID
CC (TFIID) COMPLEX THAT ARE ESSENTIAL FOR MEDIATING REGULATION OF RNA
CC POLYMERASE TRANSCRIPTION. TAFII-150 IS AN ESSENTIAL SUBUNIT WHICH
CC INTERACTS DIRECTLY WITH TBP AND TAFII-250 AND BINDS TO CORE
CC PROMOTOR DNA.
CC -1- SUBUNIT: TFIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A
CC NUMBER OF TBP-ASSOCIATED FACTORS (TAFs).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: TO YEAST TAFII-150 (TSM1).
CC
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CC
DR EMBL: X79243; CAA55830.1;
DR MEROPS: M01.UNW;
DR TRANSFAC; T02120;
DR FlyBase; FBgn0011836; Tafi150.
DR InterPro: IPR001930; Ala_peptase.
DR Pfam: PF01433; Peptidase_M1; 1.
KW Transcription regulation; Nuclear protein.
FT DOMAIN 845 1213 BINDS TO TBP AND TAFII-250.
FT DOMAIN 1138 1183 HIGHLY CHARGED.
SQ SEQUENCE 1213 AA; 139533 MW; 72A5B473E26FD064 CRC64;

Query Match 54.8%; Score 46; DB 1; Length 1213;
Best Local Similarity 53.3%; Pred. No. 15;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDTPPLWIKTE 15
DB 620 LKAMDSPVLWIRLD 634

RESULT 4
YASB_SCHPO
ID YASB_SCHPO STANDARD; PRT; 777 AA.
AC Q10146;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C3H8.11 in chromosome I.
GN SPAC3H8.11 OR SPAC1F3.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,

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CC -----
CC EMBL: U94887; AAC40586.1; -.
CC KW Transferase; Nucleotidyltransferase; RNA-directed RNA polymerase.
SQ SEQUENCE 1305 AA; 150293 MW; 3A1E9E7FCF6F11A CRC64;
-----
Query Match      52.4%; Score 44; DB 1; Length 1305;
Best Local Similarity 50.0%; Pred. NO. 34;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY | 1 LKAMDPTPPLWIKT 14
   | :|:|:||||:|
Db 960 VKLIDQSPPLWNET 973
-----
RESULT 6
NAGZ_SALT1 STANDARD; PRT; 341 AA.
AC Q8Z7I6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Beta-hexosaminidase (EC 3.2.1.52) (N-acetyl-beta-glucosaminidase)
DN (Beta-N'-acetylhexosaminidase).
GE NAGZ OR STYL249.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
ON NCBI_TAXID=601;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jageis K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
CC -1- FUNCTION: Cleaves GlcNAc linked beta-1,4 to MurNAc tripeptides (By similarity).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-acetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides.
CC -1- PATHWAY: Cell wall synthesis; murein tripeptide recycling pathway.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES. NAGZ SUBFAMILY.
CC -----
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CC -----
CC EMBL: AL627269; CAD08333.1; -.
CC DR InterPro; IPR001764; GH_3N.
CC DR Pfam; PF00933; Glyco.hydro.3.1.
CC DR PROSITE; PS00775; GLYCOSYL_HYDROL_F3; 1.
KW Hydrolase; Glycosidase; Peptidoglycan synthesis; Cell division;
KW Cell wall; Complete proteome.
FT ACT_SITE 248 248 BY SIMILARITY.
SQ SEQUENCE 341 AA; 37668 MW; 0E7F334868371800 CRC64;
```

Query Match 51.2%; Score 43; DB 1; Length 341;  
Best Local Similarity 47.1%; Pred. No. 12;  
Matches 8; Conservative 3; Mismatches 2; Indels 4; Gaps 1;

QY 2 KAMDPTP---PLWIKT 14  
DB 217 RAIDPRPASGSPYWLKT 233

## RESULT 7

NAGZ\_SALTY STANDARD; PRT; 341 AA.  
AC Q82Q06;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DE Beta-hexosaminidase (EC 3.2.1.52) (N-acetyl-beta-glucosaminidase)  
DE (Beta-N-acetylhexosaminidase).  
GN NAGZ OR SPW1209.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Salmonella.  
OX NCBI\_TaxID=602;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LT2 / SGSC1412 / ATCC 700720;  
RX MEDLINE=21534948; PubMed=11677609;  
RA McClelland M., Anderson K.E., Spieth J., Clifton S.W., Latreille P.,  
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
RA Waterston R., Wilson R.K.;  
RT \*Complete genome sequence of Salmonella enterica serovar Typhimurium  
LT2.\*;  
RL Nature 413:852-856(2001).  
CC -|- FUNCTION: Cleaves GlcNAc linked beta-1,4 to MurNAc tripeptides (By  
CC similarity).  
CC -|- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-  
CC acetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides.  
CC -|- PATHWAY: Cell wall synthesis; murein tripeptide recycling pathway.  
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -|- SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES. NAGZ  
CC SUBFAMILY.

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EMBL; AE008752; AAL20138.1;  
DR StyGene; SG77777; nagz.  
DR InterPro; IPR001764; GH\_3N.  
DR Pfam; PF00933; Glyco\_hydro\_3; 1.  
DR PROSITE; PS00775; GLYCOSYL\_HYDROL\_F3; 1.  
KW Hydrolase; Glycosidase; Peptidoglycan synthesis; Cell division;  
FT Cell wall; Complete proteome.  
FT ACT\_SITE 248 248  
SQ SEQUENCE 341 AA; 37698 MW; E07E83487336A300 CRC64;

Query Match 51.2%; Score 43; DB 1; Length 341;  
Best Local Similarity 47.1%; Pred. No. 12;  
Matches 8; Conservative 3; Mismatches 2; Indels 4; Gaps 1;

QY 2 KAMDPTP---PLWIKT 14  
DB 217 RAIDPRPASGSPYWLKT 233

## RESULT 8

HMDH\_STRPU

HMDD\_STRPU STANDARD; PRT; 932 AA.  
AC P16393;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34) (HMG-CoA  
DE reductase).  
OS Strongylocentrotus purpuratus (Purple sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;  
OC Strongylocentrotus.  
OX NCBI\_TaxID=7668;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89054023; PubMed=3192541;  
RA Woodward H.D., Allen J.M.C., Lennarz W.J.;  
RT \*3-hydroxy-3-methylglutaryl-coenzyme A reductase of the sea urchin  
RT embryo. Deduced structure and regulatory properties.\*;  
RL J. Biol. Chem. 263:18411-18418(1988).  
RN [2]  
RP SEQUENCE OF 689-735 FROM N.A.  
RX MEDLINE=88115403; PubMed=3276692;  
RA Woodward H.D., Allen J.M.C., Lennarz W.J.;  
RT \*3-hydroxy-3-methylglutaryl coenzyme A reductase in the sea urchin  
RT embryo is developmentally regulated.\*;  
RL J. Biol. Chem. 263:2513-2517(1988).  
CC -|- FUNCTION: THIS TRANSMEMBRANE GLYCOPROTEIN IS INVOLVED IN THE  
CC CONTROL OF CHOLESTEROL BIOSYNTHESIS. IT IS THE RATE-LIMITING  
CC ENZYME OF STEROL BIOSYNTHESIS.  
CC -|- CATALYTIC ACTIVITY: (R)-mevalonate + CoA + 2 NADP(+) -> (S)-3-  
CC hydroxy-3-methylglutaryl-CoA + 2 NADPH.  
CC -|- PATHWAY: Cholesterol biosynthesis.  
CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
CC reticulum.  
CC -|- SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY.

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CC -----

EMBL; J04200; AAA30060.1;  
DR EMBL; J03523; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A28367; A28367.  
DR PIR; A31898; A31898.  
DR InterPro; IPR002202; HMG-CoA\_red.  
DR InterPro; IPR000731; HMGCR/patch\_5TM.  
DR InterPro; IPR004554; HMG-CoA\_R\_NADP.  
DR InterPro; IPR004816; HMG-CoA\_red.  
DR Pfam; PF00368; HMG-CoA\_red; 1.  
DR PRINTS; PR00071; HMGCOARDFASE.  
DR TIGRfams; TIGR00533; HMG-CoA\_R\_NADP; 1.  
DR TIGRfams; TIGR00920; 2A060605; 1.  
DR PROSITE; PS00066; HMG\_COA\_REDUCTASE\_1; 1.  
DR PROSITE; PS00318; HMG\_COA\_REDUCTASE\_2; 1.  
DR PROSITE; PS01192; HMG\_COA\_REDUCTASE\_3; 1.  
DR PROSITE; PS50065; HMG\_COA\_REDUCTASE\_4; 1.  
DR PROSITE; PS50156; SSD; 1.  
KW Oxidoreductase; Glycoprotein; Endoplasmic reticulum; Transmembrane;  
KW Cholesterol biosynthesis; NADP.  
FT DOMAIN 1 338  
FT DOMAIN 339 467  
FT DOMAIN 468 932  
FT ACT\_SITE 575 575  
FT ACT\_SITE 783 783  
FT ACT\_SITE 882 882  
FT CARBOHYD 279 279  
FT CARBOHYD 850 850  
FT CARBOHYD 886 886  
SQ SEQUENCE 932 AA; 100965 MW; A645677DE1142A7B CRC64;

Query Match 51.28; Score 43; DB 1; Length 932;  
 Best Local Similarity 70.08; Pred. No. 34;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KANDPTPLW 11  
 DB 298 KKIDPTPLW 307

RESULT 9  
 Y306\_CHLMU Y306\_CHLMU STANDARD; PRT; 398 AA.  
 AC Q3PL02;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein TC0306.  
 GN TC0306.  
 OS Chlamydia muridarum.  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=83560;  
 RN [1]

SEQUENCE FROM N.A.  
 RC STRAIN=MOPn / Nigg;  
 RX MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
 RA Winn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
 RA Eisen J., Fraser C.M.;  
 RA "Genome sequences of Chlamydia trachomatis MOPn and Chlamydia  
 RT pneumoniae AR39.";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0129/CT036/TC0306  
 CC FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@lsb-sib.ch](mailto:license@lsb-sib.ch)).  
 CC -----  
 CC ENBL: AE002298; AAF39171.1;  
 DR TIGR: TC0306;  
 DR KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 31 51 POTENTIAL.  
 FT TRANSMEM 56 76 POTENTIAL.  
 SQ SEQUENCE 398 AA; 44639 MW; 8CD8E541C5C92A88 CRC64;

Query Match 50.08; Score 42; DB 1; Length 398;  
 Best Local Similarity 77.88; Pred. No. 20;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KANDPTPLW 10  
 DB 309 KELDPTPLW 317

RESULT 10  
 AAT5\_ARATH AAT5\_ARATH STANDARD; PRT; 453 AA.  
 AC P46248; O49392;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Aspartate aminotransferase, chloroplast precursor (EC 2.6.1.1)  
 DE (Transaminase A).  
 GN ASP5 OR AAT1 OR AT4G31990 OR F10N7.200.  
 OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]

SEQUENCE FROM N.A.  
 RC STRAIN=cv. C24; TISSUE=Leaf;  
 RX MEDLINE=9524373; PubMed=7766905;  
 RA Wilkie S.E., Roper J.M., Smith A.G., Warren M.J.;  
 RA "Isolation, characterisation and expression of a cDNA clone encoding  
 RT plastid aspartate aminotransferase from Arabidopsis thaliana.";  
 RL Plant Mol. Biol. 27:1227-1233(1995).  
 RN [2]

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 RA Antonou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,  
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,  
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,  
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,  
 RA Chen E., Marra M., Martienssen R., McCombie W.R.;  
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis  
 RL thaliana";  
 RN Nature 402:769-777(1999).  
 RN [4]

SEQUENCE FROM N.A.  
 RC STRAIN=cv. Landsberg erecta; TISSUE=Leaf;  
 RX MEDLINE=97079275; PubMed=8921007;  
 RA Wilkie S.E., Lambert R., Warren M.J.;  
 RA "Chloroplastic aspartate aminotransferase from Arabidopsis thaliana:  
 RT an examination of the relationship between the structure of the gene  
 RL and the spatial structure of the protein.";  
 RN Biochem. J. 319:969-976(1996).  
 RN [3]

SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=20083488; PubMed=10617198;  
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,  
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,  
 RA Harris B., Absorge W., Brandt P., Grivell L.A., Rieger M.,  
 RA Weichselgather M., de Simone V., Obermaier B., Mächer R., Mueller M.,  
 RA Kreis W., Delzeny M., Puigdomenech P., Watson M., Schmidheini T.,  
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,  
 RA Vos P., Hohenseil J., Zimmermann W., Wedler H., Ridley P.,  
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,  
 RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,  
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,  
 RA Weitzenecker T., Bothe G., Ramsperger U., Hilbert H., Braun M.,  
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,  
 RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,  
 RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,  
 RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,  
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,  
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Mayes R.,  
 RA Pettitt A., Fajandream M.A., Lyne M., Benes V., Rechmann S.,  
 RA Borkova D., Eloecker H., Scharfe M., Grimm M., Loechnert T.-H.,  
 RA Dose S., de Eaan M., Maarse A.C., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fartmann B., Grandrath K., Dauner D., Herzi A.,  
 RA Neumann S., Argirion A., Vitale D., Liguori R., Piravandi E.,  
 RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,  
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,  
 RA Chedori F., Cooke R., Berger C., Monfort A., Casacuberta E.,  
 RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,  
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,  
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielek C.,  
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,  
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,  
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,  
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,  
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,  
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,  
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,  
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,  
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,  
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,  
 RA Antonou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,  
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,  
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,  
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,  
 RA Chen E., Marra M., Martienssen R., McCombie W.R.;  
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis  
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 RA Wilkie S.E., Lambert R., Warren M.J.;  
 RA "Chloroplastic aspartate aminotransferase from Arabidopsis thaliana:  
 RT an examination of the relationship between the structure of the gene  
 RL and the spatial structure of the protein.";  
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SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=20083488; PubMed=10617198;  
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,  
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,  
 RA Harris B., Absorge W., Brandt P., Grivell L.A., Rieger M.,  
 RA Weichselgather M., de Simone V., Obermaier B., Mächer R., Mueller M.,  
 RA Kreis W., Delzeny M., Puigdomenech P., Watson M., Schmidheini T.,  
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,  
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 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,  
 RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,  
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,  
 RA Weitzenecker T., Bothe G., Ramsperger U., Hilbert H., Braun M.,  
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,  
 RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,  
 RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,  
 RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,  
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,  
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Mayes R.,  
 RA Pettitt A., Fajandream M.A., Lyne M., Benes V., Rechmann S.,  
 RA Borkova D., Eloecker H., Scharfe M., Grimm M., Loechnert T.-H.,  
 RA Dose S., de Eaan M., Maarse A.C., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fartmann B., Grandrath K., Dauner D., Herzi A.,  
 RA Neumann S., Argirion A., Vitale D., Liguori R., Piravandi E.,  
 RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,  
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,  
 RA Chedori F., Cooke R., Berger C., Monfort A., Casacuberta E.,  
 RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,  
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,  
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielek C.,  
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,  
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,  
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,  
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,  
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,  
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,  
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,  
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,  
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,  
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,  
 RA Antonou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,  
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,  
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,  
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,  
 RA Chen E., Marra M., Martienssen R., McCombie W.R.;  
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis  
 RL thaliana";  
 RN Nature 402:769-777(1999).  
 RN [4]

SEQUENCE FROM N.A.  
 RC STRAIN=cv. Landsberg erecta; TISSUE=Leaf;  
 RX MEDLINE=97079275; PubMed=8921007;

RC STRAIN-cv. Columbia;  
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the  
SSP consortium (Salk/Stanford/PGEC).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: IMPORTANT FOR THE METABOLISM OF AMINO ACIDS AND KREBS-  
CYCLE RELATED ORGANIC ACIDS. IN PLANTS, IT IS INVOLVED IN NITROGEN  
CC METABOLISM AND IN ASPECTS OF CARBON AND ENERGY METABOLISM.  
CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate -> oxaloacetate +  
L-glutamate.  
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Chloroplast.  
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
CC AMINOTRANSFERASES.  
CC  
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CC  
CC EMBL; X81026; CAA56932.1; -  
CC EMBL; X91865; CAA62972.1; -  
CC EMBL; AL021636; CAA16590.1; -  
CC EMBL; AL161580; CAB79917.1; -  
CC EMBL; AY054660; AAK96851.1; -  
CC HSSP; P00508; 7AAT.  
CC InterPro: IPR004839; AminoTransf1/2.  
CC InterPro: IPR000796; AsptTransf\_sub.  
CC InterPro: IPR004838; NTransf\_1.  
CC Pfam; PF00155; aminotran\_1\_2; 1.  
CC PRINTS; PR00799; TRANSAMINASE.  
CC PROSITE; PS00105; AA\_TRANSF\_CLASS\_1; 1.  
CC Transfaser; AminoTransferase; Pyridoxal phosphate; Chloroplast;  
KW Transit peptide; Multigene family.  
FT TRANSIT 1 52 CHLOROPLAST (POTENTIAL).  
FT CHAIN 53 453 ASPARTATE AMINOTRANSFERASE.  
FT BINDING 298 298 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
FT CONFLICT 22 23 KL -> NV (IN REF. 1 AND 2).  
SQ SEQUENCE 453 AA; 49831 MW; D3389C6FB0C4ADC CRC64;  
  
Query Match 50.0%; Score 42; DB 1; Length 453;  
Best Local Similarity 60.0%; Pred. No. 23;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 MDPTPLWIK 13  
DB 238 IDPTPEQVVK 247  
  
RESULT 11  
NCAP\_MACHU  
ID NCAP\_MACHU STANDARD; PRT; 564 AA.  
AC P26576;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Nucleocapsid protein (Nucleoprotein).  
GN N.  
OS Machupo virus.  
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.  
OX NCBI\_TaxID=111628;  
CC [1]  
CC SEQUENCE FROM N.A.  
CC STRAIN-AA288-77;  
CC MEDLINE-92296904; PubMed-1318712;  
CC Griffiths C., Wilson S.W., Clegg J.C.S.;  
CC "Sequence of the nucleocapsid protein gene of Machupo virus: close  
CC relationship with another South American pathogenic arenavirus,  
CC Junin.";  
CC  
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CC  
CC EMBL; X81026; CAA56932.1; -  
CC EMBL; X91865; CAA62972.1; -  
CC EMBL; AL021636; CAA16590.1; -  
CC EMBL; AL161580; CAB79917.1; -  
CC EMBL; AY054660; AAK96851.1; -  
CC HSSP; P00508; 7AAT.  
CC InterPro: IPR004839; AminoTransf1/2.  
CC InterPro: IPR000796; AsptTransf\_sub.  
CC InterPro: IPR004838; NTransf\_1.  
CC Pfam; PF00155; aminotran\_1\_2; 1.  
CC PRINTS; PR00799; TRANSAMINASE.  
CC PROSITE; PS00105; AA\_TRANSF\_CLASS\_1; 1.  
CC Transfaser; AminoTransferase; Pyridoxal phosphate; Chloroplast;  
KW Transit peptide; Multigene family.  
FT TRANSIT 1 52 CHLOROPLAST (POTENTIAL).  
FT CHAIN 53 453 ASPARTATE AMINOTRANSFERASE.  
FT BINDING 298 298 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
FT CONFLICT 22 23 KL -> NV (IN REF. 1 AND 2).  
SQ SEQUENCE 453 AA; 49831 MW; D3389C6FB0C4ADC CRC64;  
  
Query Match 50.0%; Score 42; DB 1; Length 453;  
Best Local Similarity 60.0%; Pred. No. 23;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 MDPTPLWIK 13  
DB 238 IDPTPEQVVK 247  
  
RESULT 12  
FASL\_SCHAM  
ID FASL\_SCHAM STANDARD; PRT; 662 AA.  
AC P10675;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE Fasciclin I precursor (FAS I) (FCN).  
GN FASL.  
OS Schistocerca americana (American grasshopper).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Orthoptera; Orthoptera; Caelifera;  
OC Acridoidea; Acrididae; Acrididae; Cyrtacanthacridinae;  
OC Schistocerca  
OX NCBI\_TaxID=7009;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-88223351; PubMed-3370670;  
RA Zinn K., McAllister L., Goodman C.;  
RT "Sequence analysis and neuronal expression of fasciclin I in  
RT grasshopper and Drosophila.";  
RL Cell 53:577-587(1988).  
RN [2]  
RP SEQUENCE OF 25-42.  
RX MEDLINE-88276943; PubMed-2839842;  
RA Snow P.M., Zinn K., Harrelson A.L., McAllister L., Schilling J.,  
RA Bastiani M.J., Makk G., Goodman C.S.;  
RT "Characterization and cloning of fasciclin I and fasciclin II  
RT glycoproteins in the grasshopper.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:5291-5295(1988).  
CC -1- FUNCTION: NEURAL CELL ADHESION MOLECULE.  
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -1- TISSUE SPECIFICITY: EXPRESSED ON DIFFERENT SUBSETS OF AXON BUNDLES  
CC (FASCICLES) IN INSECT EMBRYOS.  
CC  
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CC  
CC EMBL; M20544; AAA29809.1; -

RL Arch. Virol. 124:371-377(1992).  
CC -1- SIMILARITY: BELONGS TO THE ARENAVIRUSES NUCLEOCAPSID PROTEIN  
CC FAMILY.  
CC  
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CC  
CC EMBL; X62616; CAA44486.1; -  
CC PIR; SI8042; VHXPV.  
CC InterPro: IPR00229; Arena\_nucleocap.  
CC Pfam; PF00843; Arena\_nucleocap; 1.  
CC ProDom; PD004728; Arena\_nucleocap; 1.  
KW Nucleocapsid.  
SQ SEQUENCE 564 AA; 63300 MW; D34C575B1A188BD8 CRC64;  
  
Query Match 50.0%; Score 42; DB 1; Length 564;  
Best Local Similarity 46.7%; Pred. No. 29;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 LKAMDPTPLWIKTE 15  
DB 368 VKILDPTNTLWLDIE 382  
  
RESULT 12  
FASL\_SCHAM  
ID FASL\_SCHAM STANDARD; PRT; 662 AA.  
AC P10675;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE Fasciclin I precursor (FAS I) (FCN).  
GN FASL.  
OS Schistocerca americana (American grasshopper).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Orthoptera; Orthoptera; Caelifera;  
OC Acridoidea; Acrididae; Acrididae; Cyrtacanthacridinae;  
OC Schistocerca  
OX NCBI\_TaxID=7009;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-88223351; PubMed-3370670;  
RA Zinn K., McAllister L., Goodman C.;  
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RA Snow P.M., Zinn K., Harrelson A.L., McAllister L., Schilling J.,  
RA Bastiani M.J., Makk G., Goodman C.S.;  
RT "Characterization and cloning of fasciclin I and fasciclin II  
RT glycoproteins in the grasshopper.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:5291-5295(1988).  
CC -1- FUNCTION: NEURAL CELL ADHESION MOLECULE.  
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -1- TISSUE SPECIFICITY: EXPRESSED ON DIFFERENT SUBSETS OF AXON BUNDLES  
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CC  
CC EMBL; M20544; AAA29809.1; -

DR PIR; A31817; A31817.  
DR PIR; A29900; A29900.  
DR InterPro; IPR000782; BIGH3\_fasciclin.  
DR Pfam; PF02469; Fasciclin; 3.  
KW Cell adhesion; Glycoprotein; Repeat; Signal; GPI-anchor.  
FT SIGNAL 1 24  
FT CHAIN 25 662 FASCICLIN I.  
FT REPEAT 37 165  
FT REPEAT 194 334  
FT REPEAT 339 483  
FT REPEAT 484 637  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 488 488 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 662 AA; 75282 MW; 1E648D139A16B816 CRC64;

Query Match 50.08; Score 42; DB 1; Length 662;  
Best Local Similarity 58.38; Pred. No. 35;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 LKAMDPTPLWI 12  
| : | |||||  
DB 104 LSELDGNPLWI 115

RESULT 13  
RS13\_MAIZE STANDARD; PRT; 151 AA.  
AC Q05761;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE 40S ribosomal protein S13.  
GN RPS13.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACC clade;  
OC Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93192530; PubMed=8448368;  
RA Joann P., Gigot C., Philipps G.;  
RT "CDNA nucleotide sequence and expression of a maize cytoplasmic  
ribosomal protein S13 gene."  
RL Plant Mol. Biol. 21:701-704(1993).  
CC -1- SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.  
CC  
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CC  
CC EMBL; X62455; CAA4311.1;  
DR PIR; S30146; S30146.  
DR MaizeDB; 65480;  
DR InterPro; IPR000589; Ribosomal\_S15.  
DR Pfam; PF00312; Ribosomal\_S15; 1.  
DR PROSITE; PS00362; RIBOSOMAL\_S15; 1.  
KW Ribosomal protein.  
SQ SEQUENCE 151 AA; 17058 MW; BBE3A9126748F629 CRC64;

Query Match 48.88; Score 41; DB 1; Length 151;  
Best Local Similarity 75.08; Pred. No. 11;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 TPPLWIKT 14

DB 21 TPPTWLKT 28  
||| | : ||

RESULT 14  
RS13\_AGABI STANDARD; PRT; 151 AA.  
AC P78571;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE 40S ribosomal protein S13.  
GN RPS13.  
OS Agaricus bisporus (Common mushroom).  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Agaricales; Agaricaceae; Agaricus.  
OX NCBI\_TaxID=5341;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Horst UI;  
RX MEDLINE=97111990; PubMed=8953726;  
RA Sonnenberg A.S.M., de Groot P.W.J., Schaap P.J., Baars J.J.P.,  
RA Visser J., van Griensven L.J.L.D.;  
RT "Isolation of expressed sequence tags of Agaricus bisporus and their  
assignment to chromosomes."  
RL Appl. Environ. Microbiol. 62:4542-4547(1996).  
CC -1- SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.  
CC  
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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X94704; CAA64365.1;  
DR InterPro; IPR000589; Ribosomal\_S15.  
DR Pfam; PF00312; Ribosomal\_S15; 1.  
DR PROSITE; PS00362; RIBOSOMAL\_S15; 1.  
KW Ribosomal protein.  
SQ SEQUENCE 151 AA; 17080 MW; D69F63461E2E04DE CRC64;

Query Match 47.68; Score 40; DB 1; Length 151;  
Best Local Similarity 75.08; Pred. No. 15;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 TPPLWIKT 14  
||| | : ||

RESULT 15  
YSCK\_YEREN STANDARD; PRT; 209 AA.  
AC Q01252;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE YOP proteins translocation protein K.  
GN YSCK.  
OS Yersinia enterocolitica.  
OC Plasmid pYV.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Yersinia.  
OX NCBI\_TaxID=630;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=439-80; Serotype O:9;  
RX MEDLINE=91317716; PubMed=1860816;  
RA Michiels T., Vanooteghem J.-C., de Rouvoit C., China B., Gustin A.,  
RA Boudry P., Cornil G.R.;  
RT "Analysis of virC, an operon involved in the secretion of Yop

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RT proteins by Yersinia enterocolitica.";
RL J. Bacteriol. 173:4994-5009(1991).
CC -|- FUNCTION: BELONGS TO AN OPERON INVOLVED IN THE TRANSLOCATION OF
CC YOP PROTEINS ACROSS THE BACTERIAL MEMBRANES OR IN THE SPECIFIC
CC CONTROL OF THIS FUNCTION.
CC -|- INDUCTION: AT 37 DEGREES CELSIUS IN THE ABSENCE OF CALCIUM.
CC -|- SIMILARITY: HIGH, WITH Y.PSEUDOTUBERCULOSIS CORRESPONDING ORF.
CC -----
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CC -----
DR EMBL; M74011; AAC37028.1; -.
DR PIR; B40049; B40049.
KW Plasmid; Virulence.
SQ SEQUENCE 209 AA; 23998 MW; 05FBDC449AABA988 CRC64;

Query Match 47.6%; Score 40; DB 1; Length 209;
Best Local Similarity 53.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY .1 LKAMDPTPLWIK 13
DB 152 LAAMEPQPQAWCK 164

Search completed: June 27, 2003, 18:02:17
Job time : 13 secs

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